

FIG. 1A

5' 11 20 29 38 47 56
 GAG ACT CAC GGT CAA GCT AAG GCG AAG AGT GGG TGG CTG AAG CCA TAC TAT TTT

 65 74 83 92 101 110
 ATA GAA TTA ATG GAA AGC AGA AAA GAC ATC ACA AAC CAA GAA GAA CTT TGG AAA

 M E S R K D I T N Q E E L W K

 119 128 137 146 155 164
 ATG AAG CCT AGG AGA AAT TTA GAA GAA GAC GAT TAT TTG CAT AAG GAC ACG GGA

 M K P R R N L E E D D Y L H K D T G

 173 182 191 200 209 218
 GAG ACC AGC ATG CTA AAA AGA CCT GTG CTT TTG CAT TTG CAC CAA ACA GCC CAT

 E T S M L K R P V L L H L H Q T A H

 227 236 245 254 263 272
 GCT GAT GAA TTT GAC TGC CCT TCA GAA CTT CAG CAC ACA CAG GAA CTC TTT CCA

 A D E F D C P S E L Q H T Q E L F P

 281 290 299 308 317 326
 CAG TGG CAC TTG CCA ATT AAA ATA GCT GCT ATT ATA GCA TCT CTG ACT TTT CTT

 70 Q W H L P I K I A A I I A S L T F L

 335 344 353 362 371 380
 TAC ACT CTT CTG AGG GAA GTA ATT CAC CCT TTA GCA ACT TCC CAT CAA CAA TAT

Y T L L R E V I H P L A T S H Q Q Y

 389 398 407 416 425 434
 TTT TAT AAA ATT CCA ATC CTG GTC ATC AAC AAA GTC TTG CCA ATG GTT TCC ATC

 F Y K I P I L V I N K V L P M V S I

 443 452 461 470 479 488
 ACT CTC TTG GCA TTG GTT TAC CTG CCA GGT GTG ATA GCA GCA ATT GTC CAA CTT

T L L A L V Y L P G V I A A I V Q L

 497 506 515 524 533 542
 CAT AAT GGA ACC AAG TAT AAG AAG TTT CCA CAT TGG TTG GAT AAG TGG ATG TTA

 H N G T K Y K K F P H W L D K W M L

 551 560 569 578 587 596
 ACA AGA AAG CAG TTT GGG CTT CTC AGT TTC TTT TTT GCT GTA CTG CAT GCA ATT

 T R K Q F G L L S F F F A V L H A I

 605 614 623 632 641 650
 TAT AGT CTG TCT TAC CCA ATG AGG CGA TCC TAC AGA TAC AAG TTG CTA AAC TGG

Y S L S Y P M R R S Y R Y K L L N W

184 185

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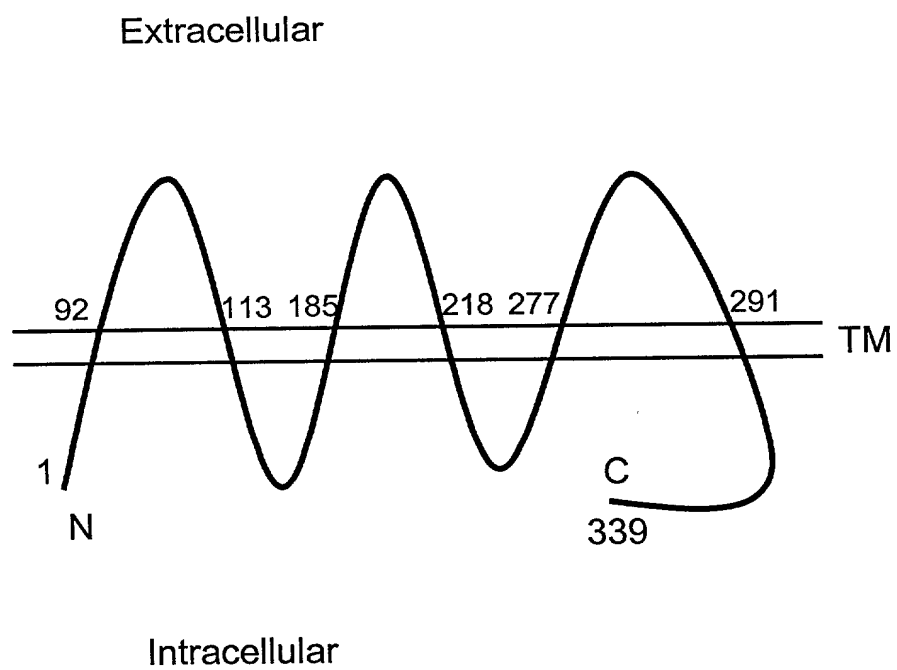
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GCA TAT CAA CAG GTC	CAA CAA AAT AAA	GAA GAT GCC TGG	ATT GAG CAT GAT	GTT	
A Y Q Q V	Q Q N K E D	A W I E H D	V		
713	722	731	740	749	758
TGG AGA ATG GAG ATT	TAT GTG TCT CTG	GGA ATT GTG GGA	TTG GCA ATA CTG	GCT	
W R M E I	Y V S L G I	V G L A I L A			
767	776	785	794	803	812
CTG TTG GCT GTG ACA	TCT ATT CCA TCT	GTG AGT GAC TCT	TTG ACA TGG	AGA GAA	
L L A V T S I P	S V S D S L T W R E				
821	830	839	848	857	866
TTT CAC TAT ATT CAG	AGC AAG CTA GGA	ATT GTT TCC CTT	CTA CTG GGC	ACA ATA	
F H Y I Q	S K L G I V S L L L	G T I			
875	884	893	902	911	920
CAC GCA TTG ATT TTT	GCC TGG AAT AAG	TGG ATA GAT ATA	AAA CAA TTT	GTA TGG	
H A L I F A W N K	W I D I K Q F V W				
929	938	947	956	965	974
TAT ACA CCT CCA ACT	TTT ATG ATA GCT	GTT TTC CTT CCA	ATT GTT GTC	CTG ATA	
Y T P P T F	M I A V F L P I V V L I				
983	992	1001	1010	1019	1028
TTT AAA AGC ATA CTA	TTC CTG CCA TGC	TTG AGG AAG AAG	ATA CTG AAG	ATT AGA	
F K S I L F L P C L	R K K I L K I R				
1037	1046	1055	1064	1073	1082
CAT GGT TGG GAA GAC	GTC ACC AAA ATT	AAC AAA ACT GAG	ATA TGT TCC	CAG TTG	
H G W E D V T K I N K T E I C S Q L					
1091	1100	1109	1118	1127	1136
TAG AAT TAC TGT TTA	CAC ACA TTT TTG	TTC AAT ATT GAT	ATA TTT TAT	CAC CAA	
* N Y C L H T F L F N I D I F Y H Q					
1145	1154	1163	1172	1181	1190
CAT TTC AAG TTT GTA	TTT GTT AAT AAA	ATG ATT ATT CAA	GGA AAA AAA AAA	AAA AAA	
H F K F V F V N K M I I Q G K K K K					

AAA AA 3'

K

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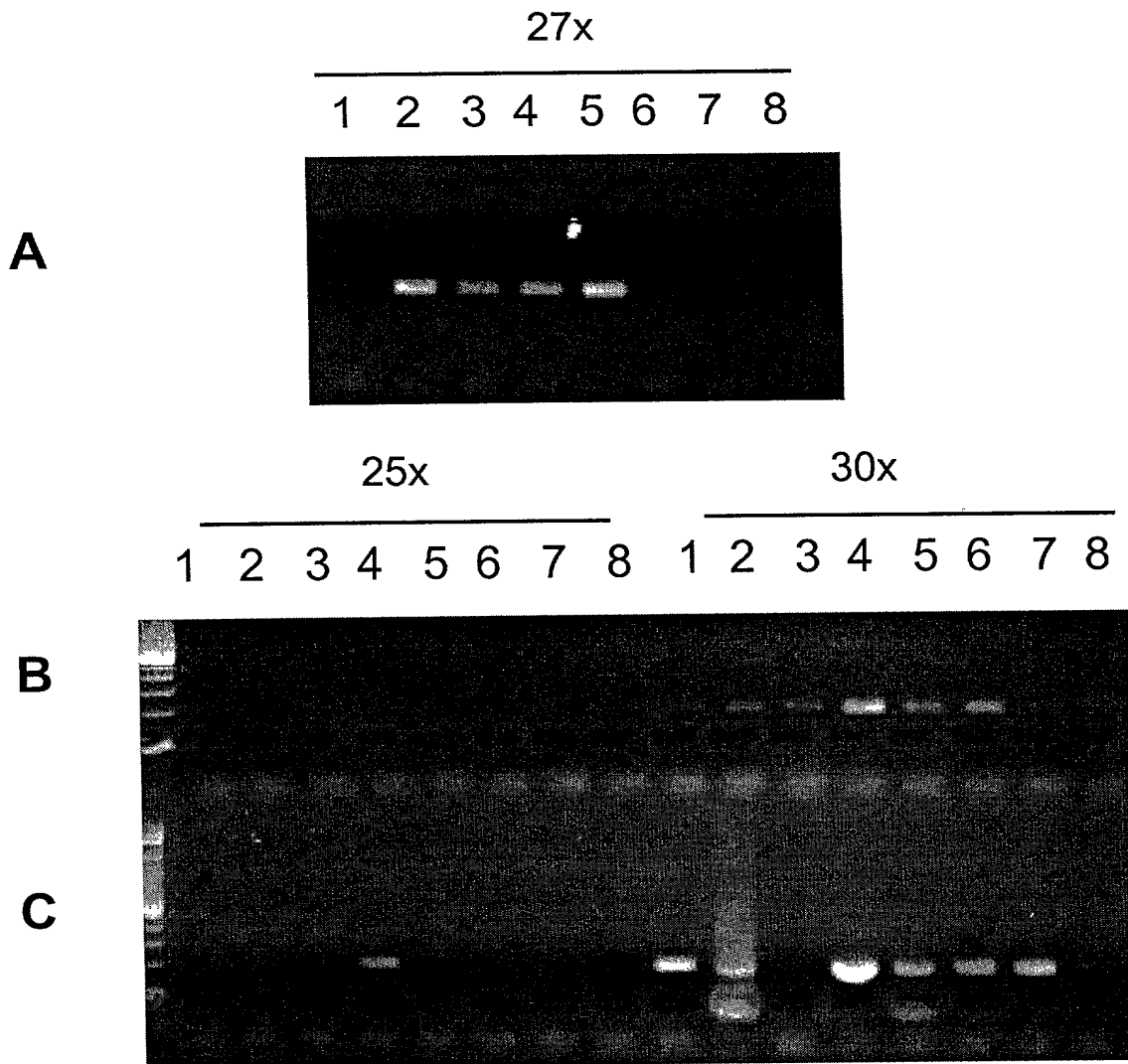
FIG. 1B



[illegible]

5'

FIG. 2



Panels:

A

1. Brain
2. Prostate
3. LAPC-4 AD
4. LAPC-4 AI
5. LAPC-9 AD
6. HeLa
7. Murine cDNA
8. Neg. control

B

1. Brain
2. Heart
3. Kidney
4. Liver
5. Lung
6. Pancreas
7. Placenta
8. Skeletal Muscle

C

1. Colon
2. Ovary
3. Leukocytes
4. Prostate
5. Small Intestine
6. Spleen
7. Testis
8. Thymus

FIG. 3A

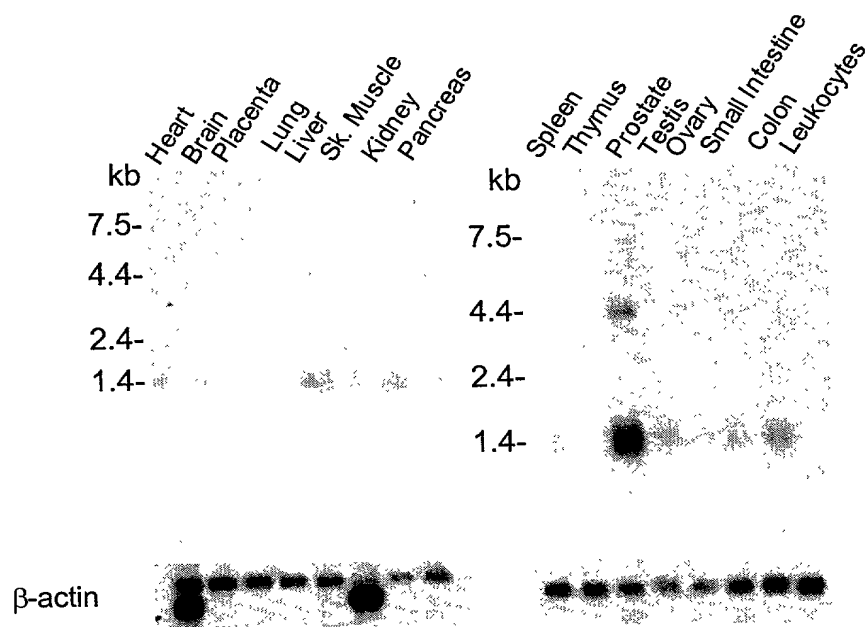
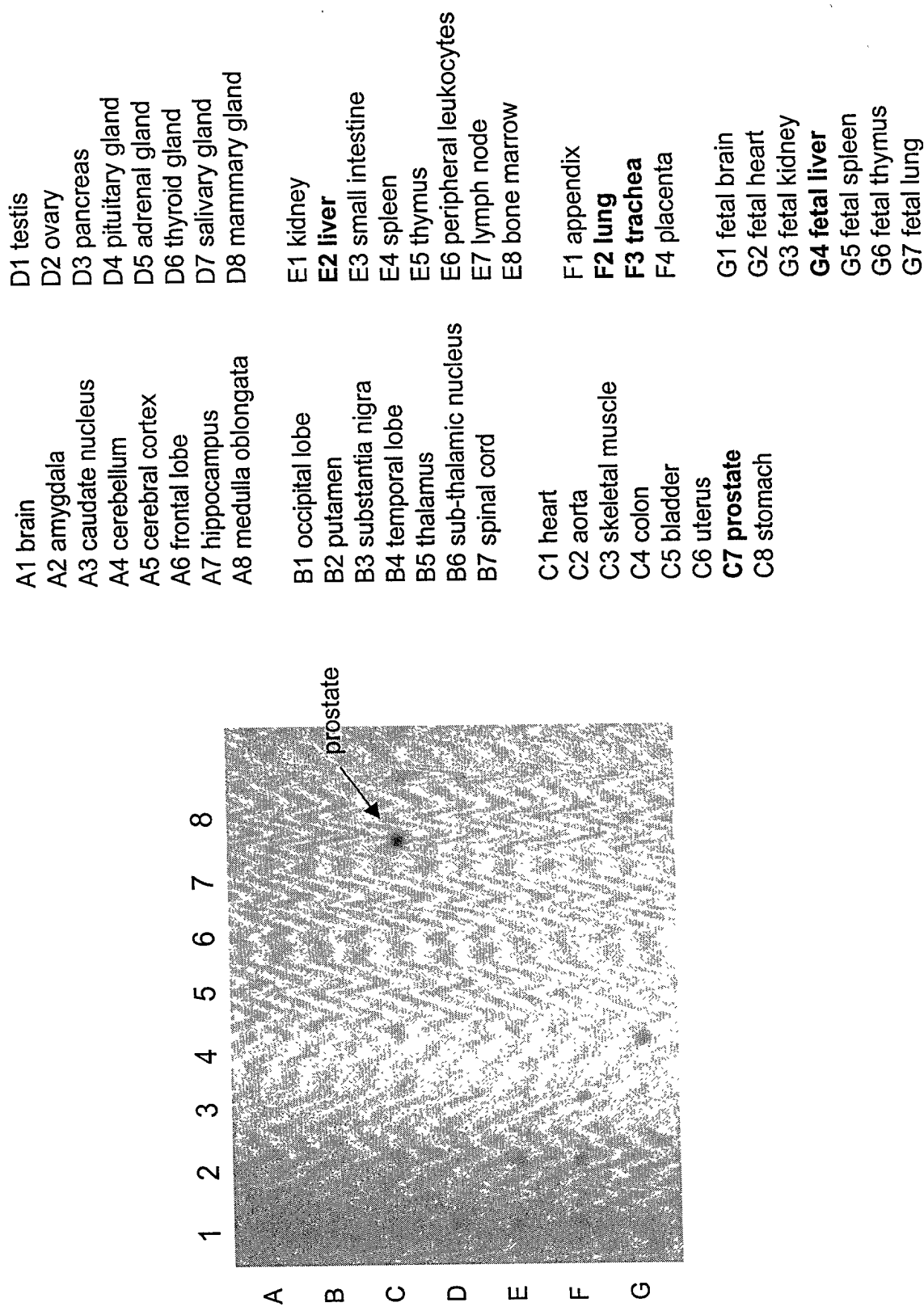


FIG. 3B



GGGGCCCGCACCTCTGGGCAGCAGCGGCAGCCGAGACTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCC
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AGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGACCTGTGCTTTTGC
ATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAACTTCAGCACACACAGGAACCTTTTCCACA
GTGGCACTTGCCAATTAAAATAGCTGCTATTATAGCATCTCTGACTTTTCTTTTACACTCTTCTGAGGGAAGTAATT
CACCCCTTAGCAACTTCCCATCAACAATATTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATGG
TTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAACCTTCATAATGGAACCAA
GTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTT
GCTGTACTGCATGCAATTTATAGTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCAT
ATCAACAGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTGTCTCT
GGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCTGTGAGTGACTCTTTGACATGG
AGAGAATTTCACTATATTCAGGTAAAATAATATATAAAATAACCCTAAGAGGTAAATCTTCTTTTTGTGTTTATGAT
ATAGAATATGTTGACTTTACCCCATAAAAAATAACAAATGTTTTTCAACAGCAAAGATCTTATACTTGTTCGAATT
AATAATGTGCTCTCCTGTGTGTTTTCCCTATTGCTTCTAATTAGGACAAGTGTTTCTTAGACATAAATAAAGGCAT
TAAATATTTCTTTGTTTTTTTTTTTTTTTGTGTTGTTTGTGTTTTGTTGTTTGTGTTTTTTTGTGATGAAGTCTCG
CTCTGTTGCCCATGCTGGAGTACAGTGGCACGATCTCGGCTCACTGCAACCTGCGCCTCCTGGGTTTCAGGCGATTCT
TCTTGCTCAGCCTCCTGAGTAGCTGGGATTACAGGCACCCATCACCATGTCCAGCTAATTTTGTATTTTGTAGTA
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CTCCATCTGAATTAGTCCAGTGTGGCTTAGAGTTGGTACAACATTCTCACAGAATTTCTTAATTTTGTAGGTTTCAG
CCTGATAACCACTGGAGTTCTTTGGTCCTCATTAAATAGCTTTCTTCACACATTGCTCTGCCTGTTACACATATGA
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1001000 "10001

FIG. 5

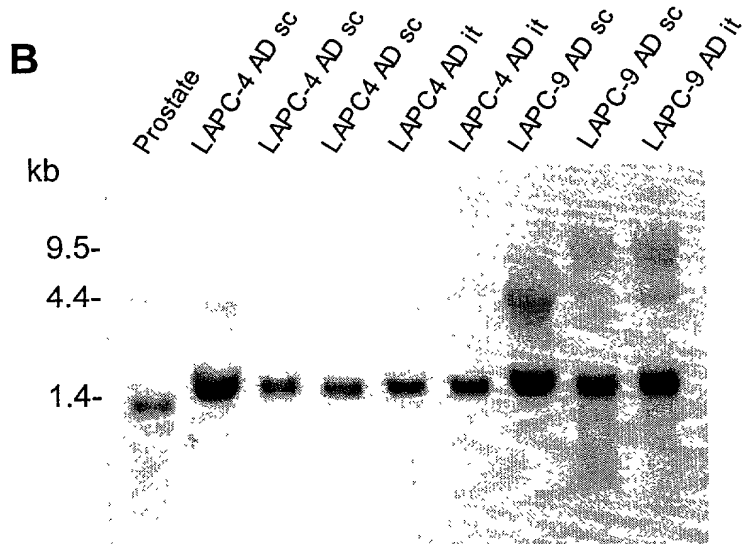
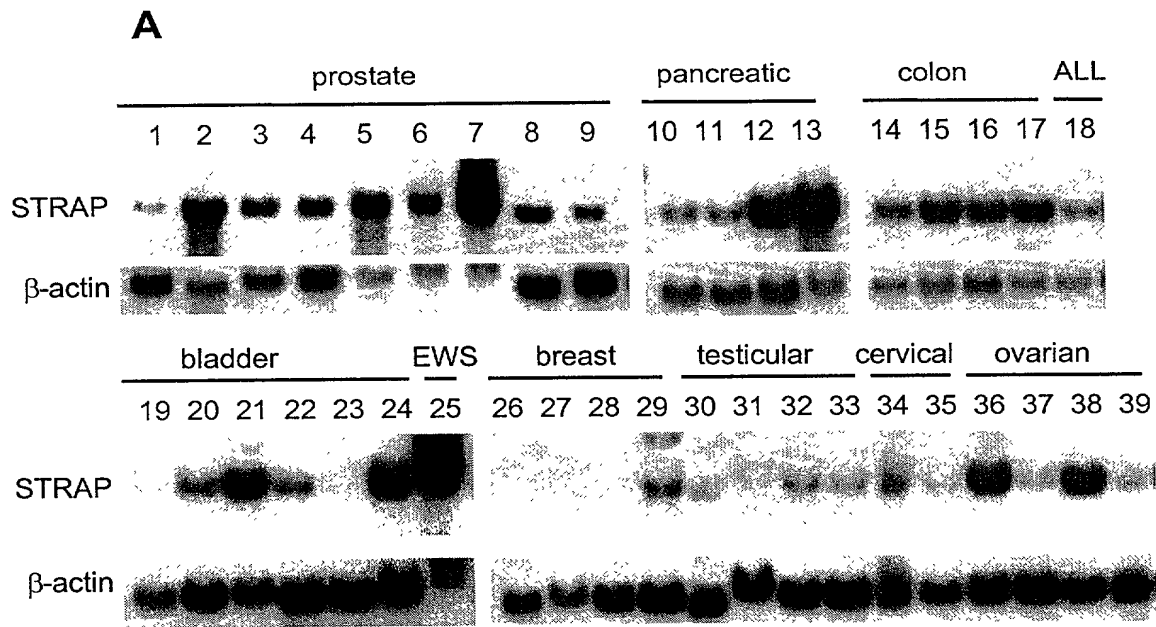
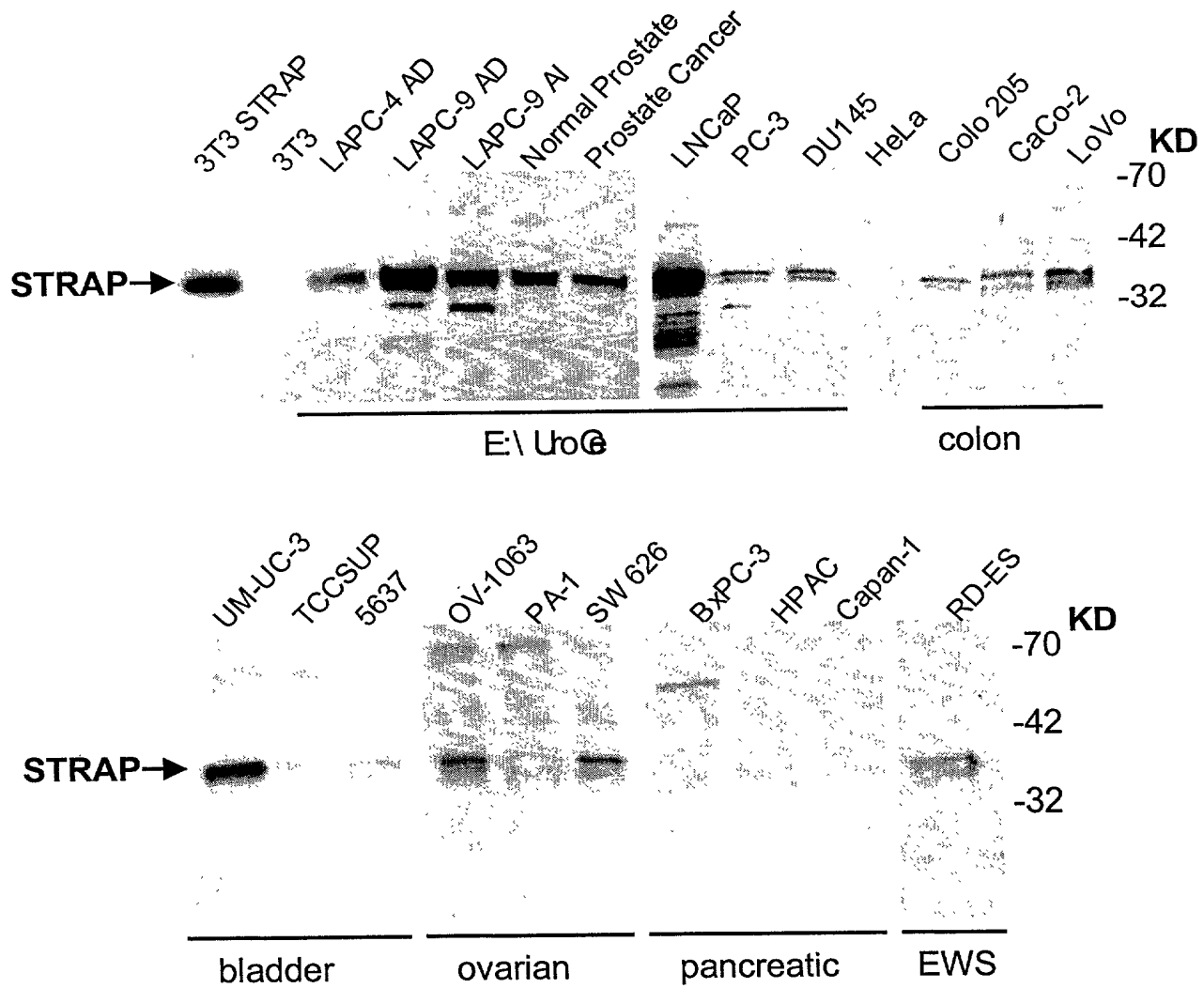


FIG. 6

FIG. 6



Year	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100																																																																																																																																																																																																
Population (millions)	1.2	1.3	1.4	1.5	1.6	1.7	1.8	1.9	2.0	2.1	2.2	2.3	2.4	2.5	2.6	2.7	2.8	2.9	3.0	3.1	3.2	3.3	3.4	3.5	3.6	3.7	3.8	3.9	4.0	4.1	4.2	4.3	4.4	4.5	4.6	4.7	4.8	4.9	5.0	5.1	5.2	5.3	5.4	5.5	5.6	5.7	5.8	5.9	6.0	6.1	6.2	6.3	6.4	6.5	6.6	6.7	6.8	6.9	7.0	7.1	7.2	7.3	7.4	7.5	7.6	7.7	7.8	7.9	8.0	8.1	8.2	8.3	8.4	8.5	8.6	8.7	8.8	8.9	9.0	9.1	9.2	9.3	9.4	9.5	9.6	9.7	9.8	9.9	10.0	10.1	10.2	10.3	10.4	10.5	10.6	10.7	10.8	10.9	11.0	11.1	11.2	11.3	11.4	11.5	11.6	11.7	11.8	11.9	12.0	12.1	12.2	12.3	12.4	12.5	12.6	12.7	12.8	12.9	13.0	13.1	13.2	13.3	13.4	13.5	13.6	13.7	13.8	13.9	14.0	14.1	14.2	14.3	14.4	14.5	14.6	14.7	14.8	14.9	15.0	15.1	15.2	15.3	15.4	15.5	15.6	15.7	15.8	15.9	16.0	16.1	16.2	16.3	16.4	16.5	16.6	16.7	16.8	16.9	17.0	17.1	17.2	17.3	17.4	17.5	17.6	17.7	17.8	17.9	18.0	18.1	18.2	18.3	18.4	18.5	18.6	18.7	18.8	18.9	19.0	19.1	19.2	19.3	19.4	19.5	19.6	19.7	19.8	19.9	20.0	20.1	20.2	20.3	20.4	20.5	20.6	20.7	20.8	20.9	21.0	21.1	21.2	21.3	21.4	21.5	21.6	21.7	21.8	21.9	22.0	22.1	22.2	22.3	22.4	22.5	22.6	22.7	22.8	22.9	23.0	23.1	23.2	23.3	23.4	23.5	23.6	23.7	23.8	23.9	24.0	24.1	24.2	24.3	24.4	24.5	24.6	24.7	24.8	24.9	25.0	25.1	25.2	25.3	25.4	25.5	25.6	25.7	25.8	25.9	26.0	26.1	26.2	26.3	26.4	26.5	26.6	26.7	26.8	26.9	27.0	27.1	27.2	27.3	27.4	27.5	27.6	27.7	27.8	27.9	28.0	28.1	28.2	28.3	28.4	28.5	28.6	28.7	28.8	28.9	29.0	29.1	29.2	29.3	29.4	29.5	29.6	29.7	29.8	29.9	30.0	30.1	30.2	30.3	30.4	30.5	30.6	30.7	30.8	30.9	31.0	31.1	31.2	31.3	31.4

Western blot analysis showing the expression of transferrin receptor and STRAP in various cell lines. The lanes are numbered 1 to 7 at the top. Molecular weight markers (KD) are indicated on the left: 70, 42, and 32. Arrows on the right point to the bands for Transferrin Receptor and STRAP. Transferrin receptor bands are visible in lanes 1, 2, 3, 4, 5, 6, and 7. STRAP bands are visible in lanes 4 and 6.

Western blot analysis showing biotinylated PCNA in various cell lines. The blot is divided into two sections. The top section shows results for 3T3 STRAP, 3T3, LNCaP, DU145, and PC-3. The bottom section shows results for UM-UC-3, TCCSUP, LOVO, and COLO. For each cell line, two lanes are shown: one with Biotin (+) and one without (-). Molecular weight markers are indicated on the left at 42 KD and 32 KD. In all cases, a strong band is visible at approximately 42 KD in the biotin (+) lanes, while the biotin (-) lanes show no signal.

FIG. 8

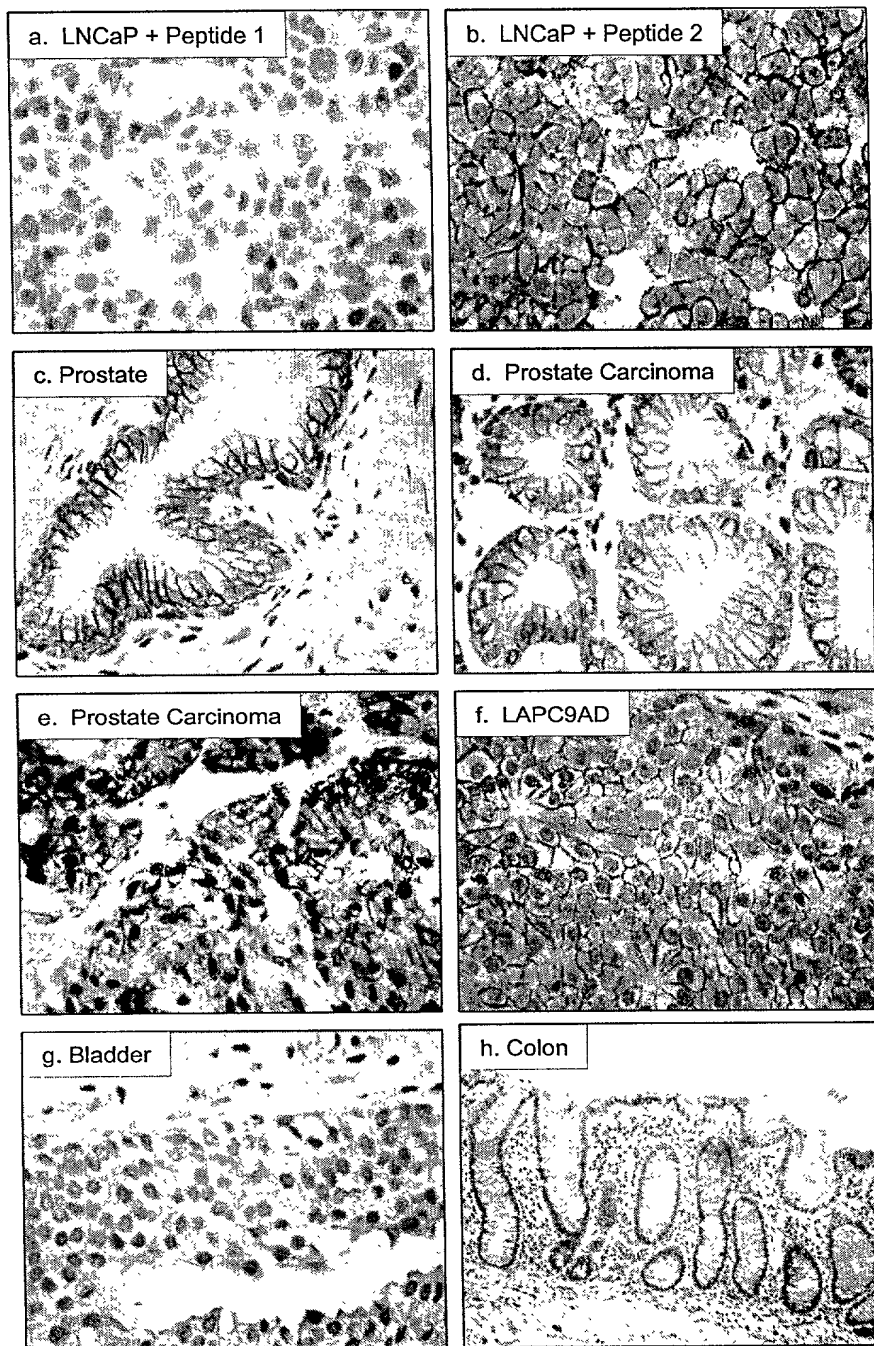


FIG. 9

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5'      10      19      28      37      46      55
GAC TTT TAC AAA ATT CCT ATA GAG ATT GTG AAT AAA ACC TTA CCT ATA GTT GCC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Asp Phe Tyr Lys Ile Pro Ile Glu Ile Val Asn Lys Thr Leu Pro Ile Val Ala

      64      73      82      91      100      109
ATT ACT TTG CTC TCC CTA GTA TAC CTC GCA GGT CTT CTG GCA GCT GCT TAT CAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Ile Thr Leu Leu Ser Leu Val Tyr Leu Ala Gly Leu Leu Ala Ala Ala Tyr Gln

      118      127      136      145      154      163
CTT TAT TAC GGC ACC AAG TAT AGG AGA TTT CCA CCT TGG TTG GAA ACC TGG TTA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Leu Tyr Tyr Gly Thr Lys Tyr Arg Arg Phe Pro Pro Trp Leu Glu Thr Trp Leu

      172      181      190      199      208      217
CAG TGT AGA AAA CAG CTT GGA TTA CTA AGT TTT TTC TTC GCT ATG GTC CAT GTT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Gln Cys Arg Lys Gln Leu Gly Leu Leu Ser Phe Phe Phe Ala Met Val His Val

      226      235      244      253      262      271
GCC TAC AGC CTC TGC TTA CCG ATG AGA AGG TCA GAG AGA TAT TTG TTT CTC AAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Ala Tyr Ser Leu Cys Leu Pro Met Arg Arg Ser Glu Arg Tyr Leu Phe Leu Asn

      280      289      298      307      316      325
ATG GCT TAT CAG CAG GTT CAT GCA AAT ATT GAA AAC TCT TGG AAT GAG GAA GAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Met Ala Tyr Gln Gln Val His Ala Asn Ile Glu Asn Ser Trp Asn Glu Glu Glu

      334      343      352      361      370      379
GTT TGG AGA ATT GAA ATG TAT ATC TCC TTT GGC ATA ATG AGC CTT GGC TTA CTT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Val Trp Arg Ile Glu Met Tyr Ile Ser Phe Gly Ile Met Ser Leu Gly Leu Leu

      388      397      406      415      424      433
TCC CTC CTG GCA GTC ACT TCT ATC CCT TCA GTG AGC AAT GCT TTA AAC TGG AGA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Ser Leu Leu Ala Val Thr Ser Ile Pro Ser Val Ser Asn Ala Leu Asn Trp Arg

      442      451      460      469      478      487
GAA TTC AGT TTT ATT CAG TCT ACA CTT GGA TAT GTC GCT CTG CTC ATA AGT ACT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Glu Phe Ser Phe Ile Gln Ser Thr Leu Gly Tyr Val Ala Leu Leu Ile Ser Thr

      496      505      514
TTC CAT GTT TTA ATT TAT GGA TGG AAA CGA GCT 3'
--- --- --- --- --- --- --- --- --- ---
Phe His Val Leu Ile Tyr Gly Trp Lys Arg Ala

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FIG. 9

FIG. 10

STRAP-2, AA508880 (NCI_CGAP Pr6)

ggtcgacttttcttttattcctttgtcagagatctgattcatccatattgctagaaaccaacagagtgactttttaca
aaattcctatagagattgtgaataaaaccttacctatagttgccattactttgctctccctagtagtaccttgagg
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cagtgtagaaaacagcttgattactaagttgtttcttcgctatggtccatggtgcctacagcctctgcttaccga
tgagaaggtcagagagat

STRAP-2, 98P4B6 SSH fragment

TTTGACGCTTTGCAGATACCCAGACTGAGCTGGAAGTGGTCTTCTCTATTGACTCTACTTCTTTAAAAGCG
GCTGCCATTACATTCTCAGCTGTCCTTGCAAGTTAGGTGTACATGTGACTGAGTGTGGCCAGTGAGATGAAGTC
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AI139607 (testis EST)

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R80991 (placental EST)

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FIG. 11A

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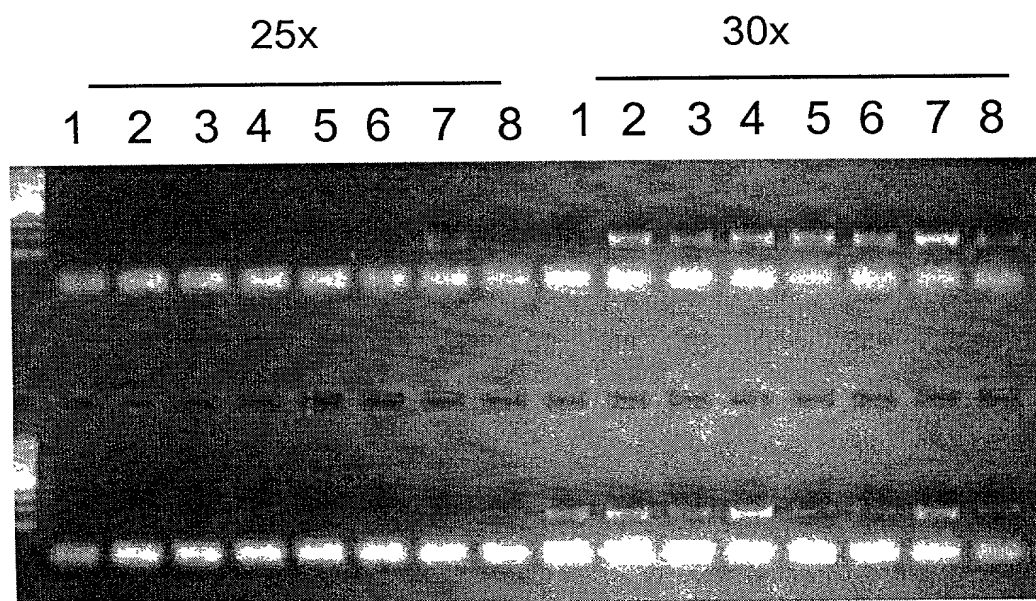
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STRAP-2      2  FYKIPIEIVNKTLPIVAITLLSLVYLAGLLAAAYQLYYGTYRRFPPWLETWLQCRKQLG
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STRAP-1     166 LLSFFFVAVLHAIYSLSPMRRSRYRYKLLNWAYQQVQONKEDAWIEHDVVRMEIYVSLGIV
STRAP-2     62  LLSFFFAMVHVAYSLCLPMRRSERYFLNMAYQQVHANIENSWNEEEVWRIEMYISFGIM
               ***** * * * * * * * * * * * * * * * * * * * * * * * *
STRAP-1     226 GLAILALLAVTSIPSVSDSLTWREFHYIQSKLGIVSLLLGTIHALIFAWNK
STRAP-2     122 SLGLLSLLAVTSIPSVSNALNWREFSFIQSTLGYVALLISTFHVLIYGWKR
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1	15	16	30	31	45	46	60	61	75	76	90										
STRAP-1	MESR	KDIT	NOEEL	WK	MKPR	NLEED	YHLK	DTGET	SMLKRP	VLLH	LHOTAH	ADEF	CPSE	LQHTQ	ELFPQW	HLPI	KIAAII	ASLTFL	YTL		
STRAP-2	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
STRAP-3	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
STRAP-4	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
91	105	106	120	121	135	136	150	151	165	166	180										
STRAP-1	LREV	IHPL	ATSHQOY	FYKIP	ILVINK	VLPM	VSI	TALALV	YIP	GVII	AAI	VQLH	NGTKY	KKF	PHWLD	KWML	TRKQ	FG	ELSSFF	FANVLHAI	YSL
STRAP-2	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
STRAP-3	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
STRAP-4	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
181	195	196	210	211	225	226	240	241	255	256	270										
STRAP-1	SYPM	RRS	RYKJ	LNNW	AYQOV	QONKED	AWIE	HDV	WRMEI	VVS	GLV	GLAI	LALL	AVTSIPS	VSD	SLTW	REPH	YIQS	KLGIV	SLDLG	THAL
STRAP-2	CLP	MRSE	RYJL	FLNNW	AYQOV	HANI	ENSMNE	EEV	WRTEM	YIS	FGIM	SLGL	LSLL	AVTSIPS	VSN	ALNW	REF	SFIQS	TGIV	VALL	STFHV
STRAP-3	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
STRAP-4	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
271	285	286	300	301	315	316	330	331	345	346	360										
STRAP-1	IFAW	NK	WIDIKQ	FVW	YTP	TFMIA	VFLPIV	VLL	FKSIL	FLP	CLRK	KILK	IRH	GWED	VTKI	NKTEI	CSQL	---	---	---	---
STRAP-2	IYGW	KRA	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
STRAP-3	YVGG	KRFL	SPSN	LRW	YLP	AAV	VLGL	IPCT	VZV	IKFV	LMP	CVDPN	TL	TEIR	QGW	ERN	SKH	---	---	---	---
STRAP-4	TYGW	TRAF	EESRY	KF	YLP	PTFT	XTL	LVPCV	RSS	WAKAL	FXL	PCIQ	P	---	---	---	---	---	---	---	---

FIG. 12



A

B

A

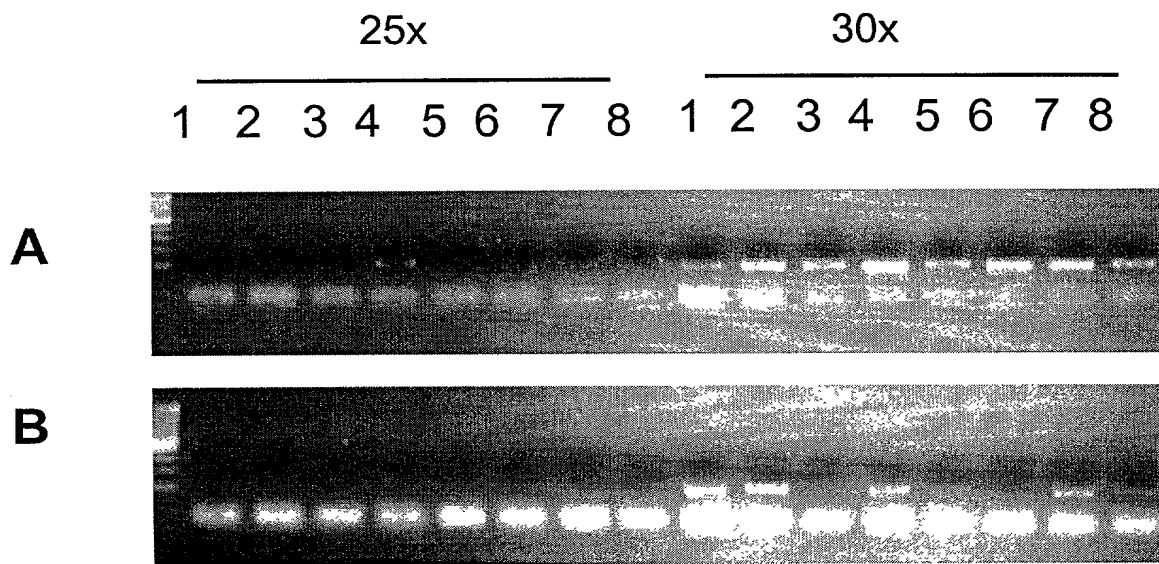
1. Brain
2. Heart
3. Kidney
4. Liver
5. Lung
6. Pancreas
7. Placenta
8. Skeletal Muscle

B

1. Colon
2. Ovary
3. Leukocytes
4. Prostate
5. Small Intestine
6. Spleen
7. Testis
8. Thymus

FIG. 13

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- A**
1. Brain
 2. Heart
 3. Kidney
 4. Liver
 5. Lung
 6. Pancreas
 7. Placenta
 8. Skeletal Muscle

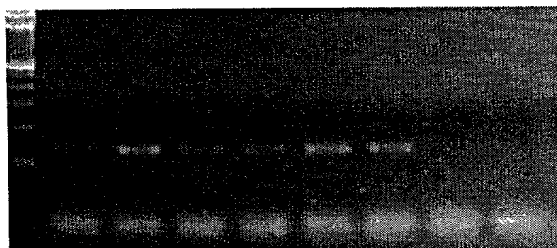
- B**
1. Colon
 2. Ovary
 3. Leukocytes
 4. Prostate
 5. Small Intestine
 6. Spleen
 7. Testis
 8. Thymus

FIG.14

26x

1 2 3 4 5 6 7 8

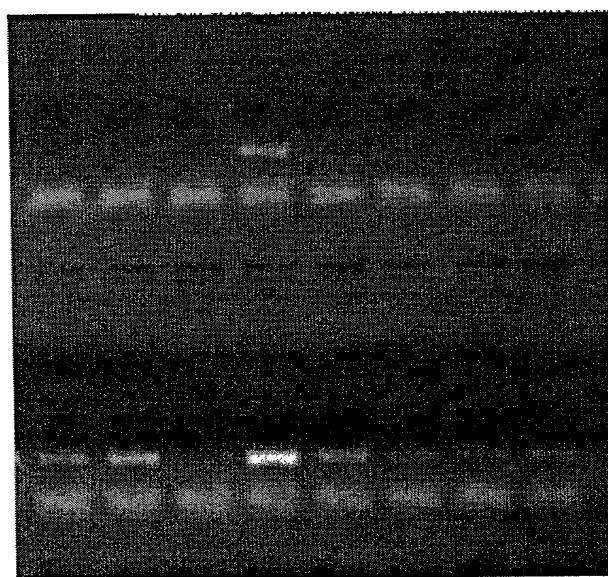
A



B

1 2 3 4 5 6 7 8

25x



30x

A

1. Brain
2. Prostate
3. LAPC-4 AD
4. LAPC-4 AI
5. LAPC-9 AD
6. HeLa
7. Murine cDNA
8. Neg. control

B

1. Colon
2. Ovary
3. Leukocytes
4. Prostate
5. Small Intestine
6. Spleen
7. Testis
8. Thymus

FIG. 15

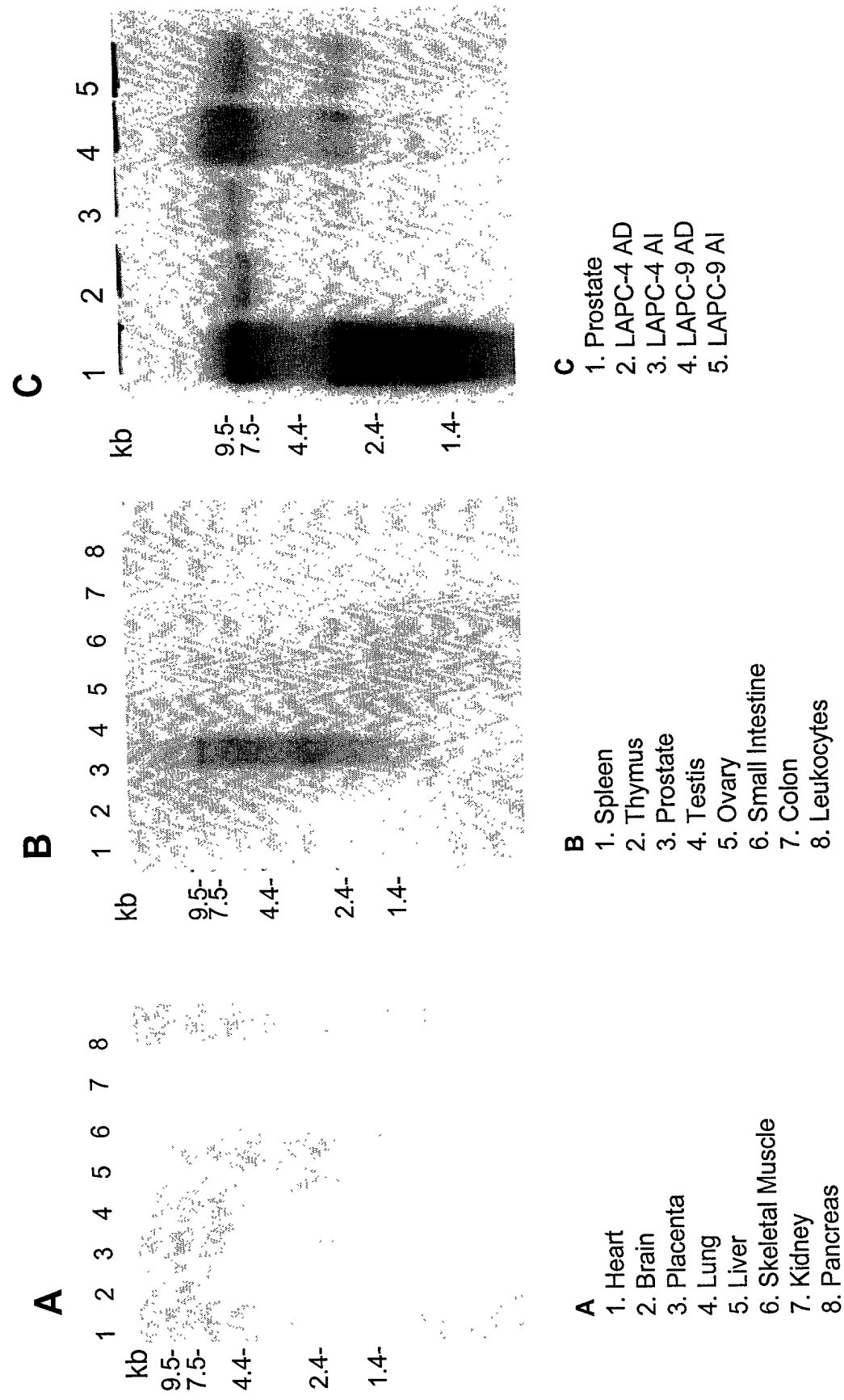
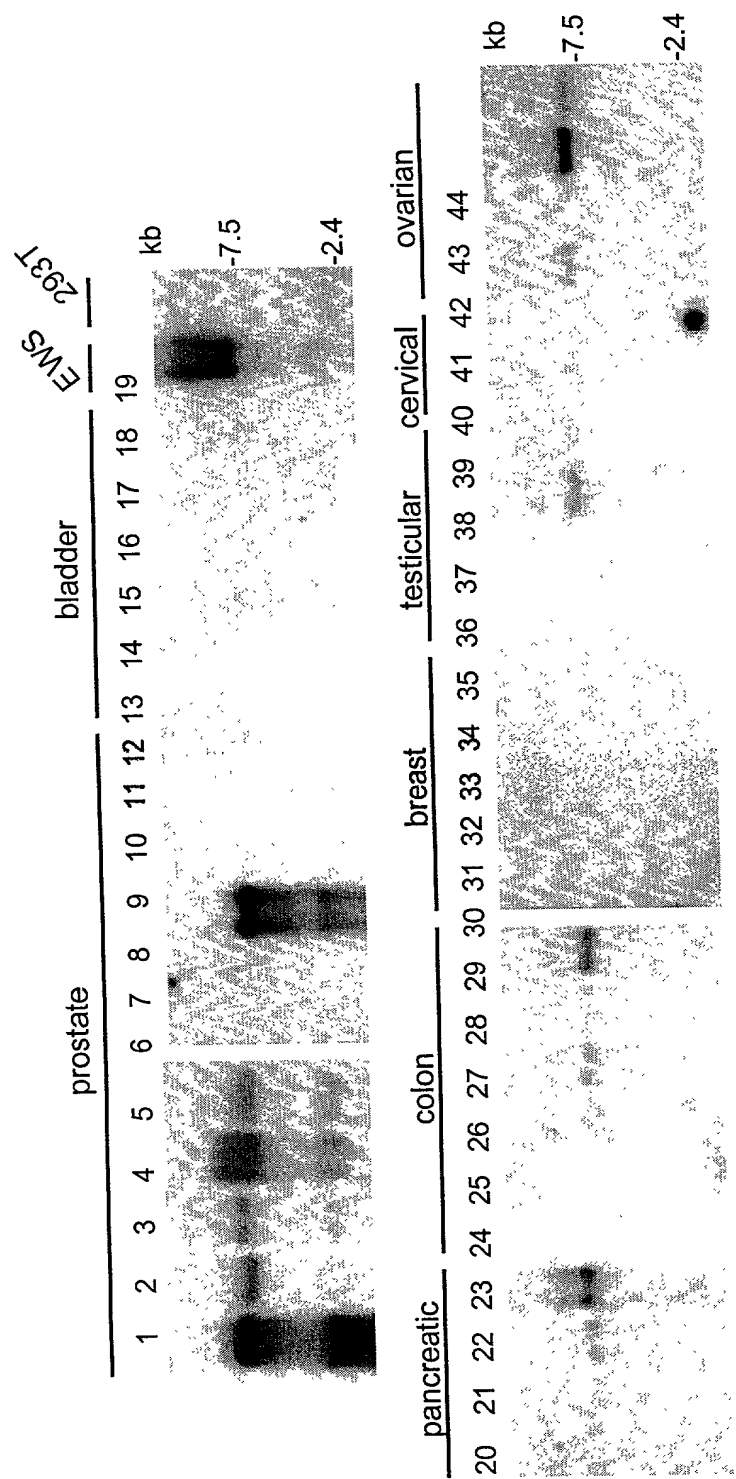


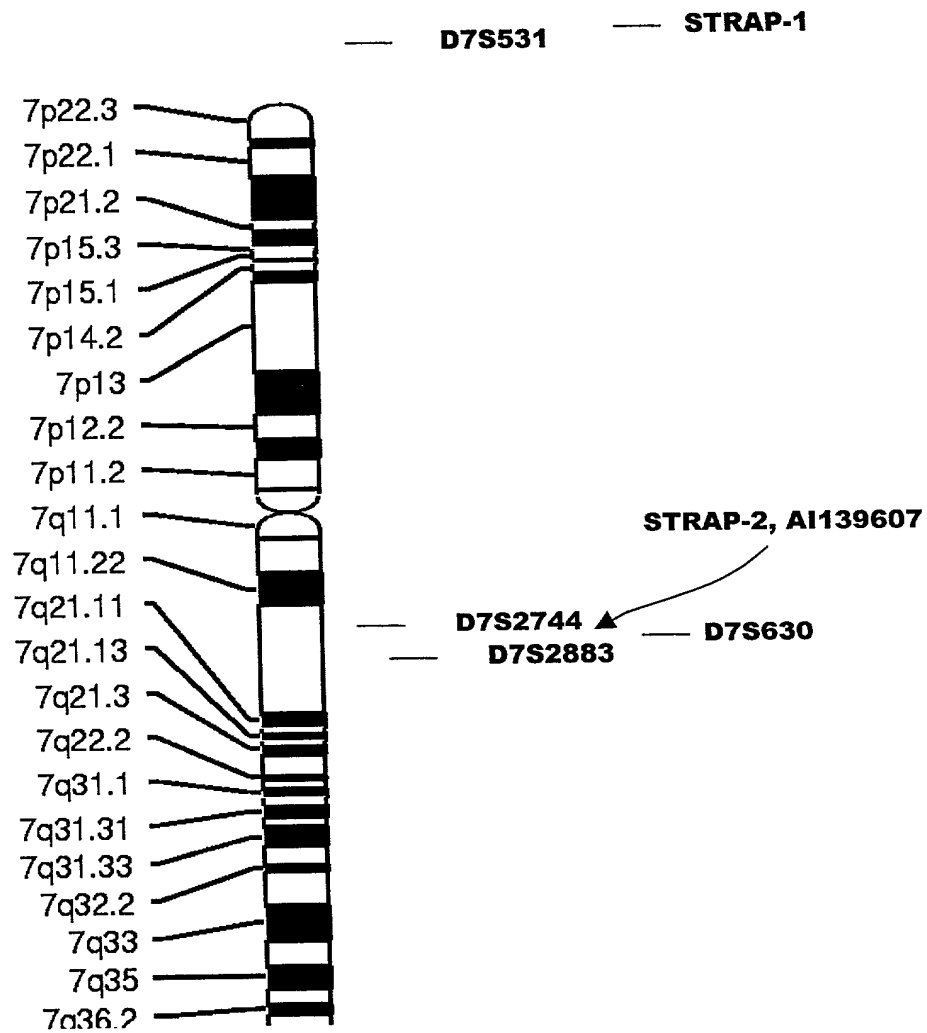
FIG. 16



- | | | |
|---------------|-----------------|-------------|
| 1. prostate | 20. PANC-1 | 39. A431 |
| 2. LAPC-4 AD | 21. BxPC-3 | 40. HeLa |
| 3. LAPC-4 AI | 22. HPAC | 41. OV-1063 |
| 4. LAPC-9 AD | 23. Capan-1 | 42. PA-1 |
| 5. LAPC-9 AI | 24. LS180 | 43. SW626 |
| 6. TsuPr1 | 25. SK-CO-1 | 44. CAO V-3 |
| 7. DU145 | 26. CaCo-2 | |
| 8. LNCaP | 27. LoVo | |
| 9. PC-3 | 28. T84 | |
| 10. LAPC-4 CL | 29. Colo-205 | |
| 11. PrEC | | |
| | 30. BT-20 | |
| | 31. CAMA-1 | |
| | 32. DU4475 | |
| | 33. MCF-7 | |
| | 34. MDA-MB-435s | |
| | 35. NTERA-2 | |
| | 36. NCCIT | |
| | 37. TERA-1 | |
| | 38. TERA-2 | |

FIG. 17

GDB Compreher



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FIG. 18

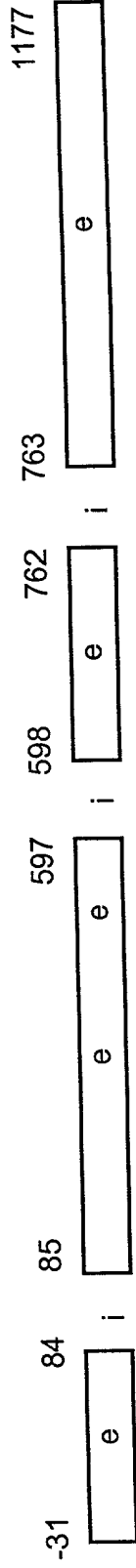
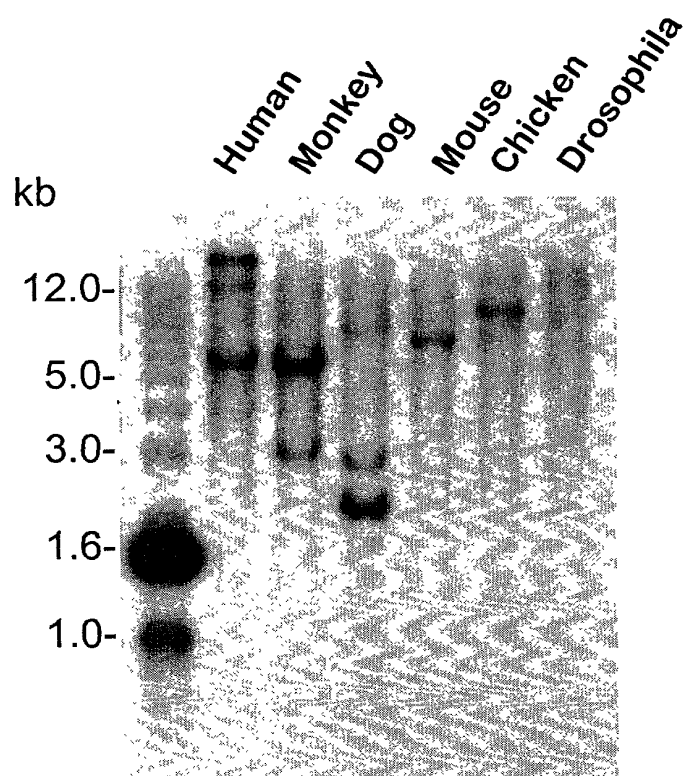
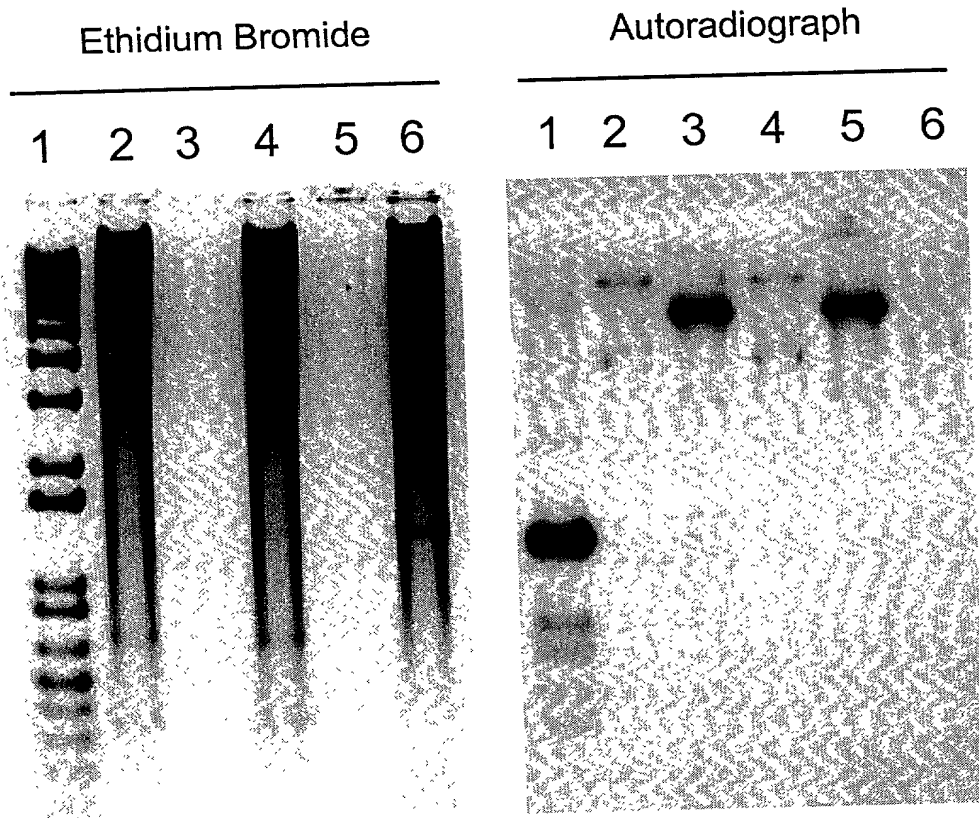


FIG. 19



10010667.120601

FIG. 20



Lanes

- 1) 1kb ladder
- 2) human female genomic
- 3) 12P11 BAC mus
- 4) human female genomic
- 5) 12P11 BAC mus
- 6) 3T3